



Quantum computation, non-demolition measurements, and reflective control in living systems

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Abstract

Internal computation underlies robust non-equilibrium living process. The smallest details of living systems are molecular devices that realize non-demolition quantum measurements. These smaller devices form larger devices (macromolecular complexes), up to living body. The quantum device possesses its own potential internal quantum state (IQS), which is maintained for a prolonged time via reflective error-correction. Decoherence-free IQS can exhibit itself by a creative generation of iteration limits in the real world. It resembles the properties of a quasi-particle, which interacts with the surround, applying decoherence commands to it. In this framework, enzymes are molecular automata of the extremal quantum computer, the set of which maintains highly ordered robust coherent state, and genome represents a concatenation of error-correcting codes into a single reflective set. The biological evolution can be viewed as a functional evolution of measurement constraints in which limits of iteration are established, possessing criteria of perfection and having selective values.

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1. Quantum non-demolition measurements in living systems

Leibniz (1965 [1714]) defined living systems as automata exceeding infinitely all artificial automata. The machines of nature, i.e. living bodies, are machines up to their smallest details ('Monadology', § 64). In modern science, the smallest details of living systems are considered as molecular automata (Marijuán and Westley, 1992) operating between the classical and the quantum levels, i.e. between the potential dimension (microscale) and the actual 3D space (macroscale). These smaller devices form larger devices (macro-

molecular complexes), up to the living body. They realize quantum measurements proceeding internally (Pattee, 1971; Igamberdiev, 1993; Matsuno, 1995).

In quantum measurements, a new actualized macrostate appears *non-locally* evolving from the previous macrostate, since its points are *not defined before* the quantum measurement. This means that quantum measurement includes a reflection to the field non-determined beforehand, i.e. it addresses a potential field at the microlevel. Since the measuring device is embedded into the system that is measured, the positions of all points are rearranged and singled out in the course of measurement. The same point taken before and after measurement becomes split into the image and its reflection. Thus, quantum measurement is a process generating a contradiction and representing a logical jump via such a contradiction

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(Gunji and Ito, 1999). This type of model can be illustrated as an *iterative algorithm*, using a dynamically changing contraction mapping as the interface of a state and a transition rule (Gunji et al., 1997). It describes a non-local structural unfolding where contradictory consequent realizations (quantum reductions) are separated within the internal time-space.

During actualization, an unaccountably infinite number of assembling states unfolds into regular series of spatial events with basically simple and reproducible structures, which selection should satisfy certain limit conditions. A limit of such recursive process originates from quantum uncertainty and corresponds to a non-local assembly, which is realized as a reduction of uncertainty in quantum measurement and described as a mapping from imaginary to real numbers (Rosen, 1977).

Reduction from the field of potentialities assumes existence of alternative realizations representing different projections into real numbers. Quantum complementarity arises as a set of these different projections that cannot exist simultaneously, where contradictory states generate the appearance of uncertainties in the coordinate/impulse or energy/time observables. When contradictory statements appearing during actualization are separated by time intervals, we sink from the mathematical into the physical world and face infinite regression avoiding simultaneous existence of opposite definitions (Igamberdiev, 1998). A separation (selection) of contradictory states occurs via measurement process. The temporal process represents as series of computable events, but, following Aristotle (Physica IV, 12, 220b), it is not our computation (by which we count) but an external natural computation (which can be counted by us, i.e. represented as an objective dependence of spatial coordinates on the time coordinate, i.e. as the physical law).

The specificity of biomacromolecules for strictly determined interactions can be explained by low energy dissipation during their operation, which provides registration of signals not distinguished by their energy from surrounding noise (Elsasser, 1982). Conformational relaxation of macromolecular systems acting as macroscopic oscillators, is considered to be an elementary action of bioenergetic process (Blumenfeld, 1983), in which the fast quantum effect (e.g. the capture of electron) is followed by a slow conformational transition during which the en-

ergy is not dissipated and remains stored for a total lifetime long enough for work to be performed. According to the Heisenberg's uncertainty ratio $\Delta E \Delta \tau \approx \hbar$, interactions between a quantum system and a macroscopic measuring device may follow a path that provides practically non-demolition registration of strictly determined weak forces (Braginsky et al., 1980). These interactions are characterized by high precision and certainty of the result of measurement, as the sensitivity of the detector is determined by its relaxation properties. These quantum non-demolition (QND) measurements are characterized by low energy dissipation (Braginsky and Khalili, 1996). They provide the basis for quantum computation by measurement (Raussendorf and Briegel, 2001; Nielsen, 2003). In the measurement model for quantum computation only two operations are required: the storage of qubits (quantum memory) and non-demolition projective measurements on up to four qubits at a time, but in the simplified models only two-qubit measurements are required (Nielsen, 2003). Also a quantum computation that consists entirely of one-qubit measurements on a particular class of entangled states has been proved to be universal (Raussendorf et al., 2003). Non-demolition measurements correspond to unitary transformations in finite dimensional Hilbert spaces (Balázs, 2003; van der Meyden and Patra, 2003).

Quantum measurement is connected with low energy dissipation in the case where the relaxation period of a macroscopic oscillator (τ^*) is many times larger than the time interval of initial quantum effect, which is measured (τ'). According to Braginsky et al. (1980), the minimal energy dissipation in quantum measurement is calculated as

$$\Delta E_{\min} \approx 2kT \left(\frac{\tau'}{\tau^*} \right)$$

This means that the value of effective temperature during conformational relaxation is decreased by the factor of (τ'/τ^*) , i.e. by many orders of magnitude, and becomes close to absolute zero. Under these conditions, internal fluctuations in the measuring device will not mask the action of weak force being detected, and specific high-frequency vibrations will be induced in the device. This is possible if the relaxation of macromolecular device keeps coherent state for a prolonged time.

Initially it was assumed that each step of computation could be equal to a measurement consuming at least $kT \ln 2$ of energy. Bennett (1979) has proved that it is possible to perform computation in such a way that expenditure of energy will be less than kT . The former should be true for the classical systems, while for details of quantum computers embodied into macromolecules it could consume as low as an order of $kT(\tau'/\tau^*)$ of energy. The minimal price of calculation (corresponding to the information of one bit) in this case could be decreased down to the value of Planck's constant (Conrad and Liberman, 1982; Liberman, 1989).

Actual energy dissipation in the course of measurement proceeds by emitting quanta, each carrying energy E at every time interval τ . It is possible to estimate the energy flow associated with measuring each quantum as carrying energy E over the time interval τ (Matsuno, 1993, 1999; Matsuno and Paton, 2000). Experiments show that the actin-activated myosin ATPase activity releases 5×10^{-13} erg of ATP energy in 10^{-2} s (Harada et al., 1990). This corresponds to slow conformation relaxation of the enzyme. The amount of quanta released in this process is calculated according to the Heisenberg's uncertainty principle as ht/E , i.e. it will be 2.2×10^6 quanta, whose typical energy is 2.2×10^{-19} erg or 1.6×10^{-3} K in temperature. This means that the effective temperature of an actomyosin complex in the presence of ATP molecules is maintained at 1.6×10^{-3} K (Matsuno and Paton, 2000). This extremely low temperature serves as means of precipitating quantum coherence.

The actin monomer moves along myosin filaments with the velocity of $10 \mu\text{m s}^{-1}$. This gives each actin monomer linear momentum 2.2×10^{-21} erg s cm^{-1} , and the corresponding de Broglie length is 4.5 nm (Matsuno and Paton, 2000), and the result is generation of molecular movements via holding quantum coherence. A similar approach for calculating energy dissipation and corresponding effective temperature will be true for any enzyme and multienzyme system (Igamberdiev, 1993, 1999a). Enzymes provide a precise specific recognition via a prolongation of the relaxation time (Igamberdiev, 1993; Matsuno, 1995), which is relevant to the QND measurement model (Braginsky et al., 1980). Enzymes decrease uncertainty in the inorganic catalysis paying by very long relaxation times according to the energy–time uncer-

tainty ratio (Igamberdiev, 1993). A specific recognition of the substrate resulting in its precise conversion is characterized by the minimum dissipation of energy. Recognition of less probable states needs longer relaxation times, which corresponds to low turnover rates of enzymes catalyzing reactions with multistep complex pathways non-occurring without catalysts, while the facilitation of simple reactions occurring easily without enzymes can be done with high turnover rates, as in the case of carbonic anhydrase or catalase.

Not only in the case of muscle contraction, but also in many other biological phenomena, the cytoskeleton may serve as an important milieu for long-distance coherence (Hameroff, 1994; Liberman et al., 1986). An initial input should cause oscillation pattern of high frequencies (10^9 to 10^{11} Hz), which will not demolish macromolecular structures (Liberman, 1979, 1989), while low-frequency conformational relaxation will follow from this initial input. Cytoskeleton may therefore serve as a three-dimensional diffraction pattern for the hypersound, which distribution results in slow conformational movements (Liberman et al., 1986).

Hameroff et al. (2002) suggested that in living systems, protein conformational states represent fundamental informational units (bits) utilized in quantum computation (qubits). In cytoskeleton, pathways for electron mobility among aromatic acids in tubulins lend themselves to topological quantum effects resistant to decoherence (Hameroff et al., 2002). Long-living coherent states in the cytoskeleton can explain non-local effects in biological function, including operation of consciousness (Hameroff and Penrose, 1996).

2. Internal quantum states of living system

Quantum computers in order to operate without errors should maintain decoherence-free subspaces via implication of error-correcting codes (Bacon et al., 1999). The living time of decoherence free subspace can be determined in frames of Heisenberg's energy–time uncertainty ratio (Igamberdiev, 1993). A continuous measurement holds a decoherence-free state via the quantum Zeno-effect between levels (Facchi and Pascazio, 2002). To perform a robust quantum computation in decoherence free subspaces, they must be supplemented with the quantum error

correcting codes (Gea-Banacloche, 2000) performing quantum feedback control. It provides perfectly measured error channel per physical qubit and stabilizes codespace (Ahn et al., 2003). As a result, the power law appears in the system, which is introduced via hyperlinks (Gödel numbers) in the set of real numbers (Igamberdiev, 2003).

Quantum computer can be protected against decoherence for an arbitrary length of time, provided a certain threshold error rate can be achieved. Encoding the state of quantum computer for error correction has the effect of making its operating states macroscopically indistinguishable: the more “stable” the code is, the more errors it can correct in each pass. The concatenated codes involve re-encoding already encoded bits. This process reduces the effective error rate at each level, with the final accuracy being dependent on how many levels of the hierarchy are used. To avoid a collapse of the quantum information in the process of correcting errors, it is possible to make a partial measurement that extracts only the error information and leaves the encoded state untouched.

Quantum error-correcting methods protect information in memory, while the concatenation involves the applying this combination of techniques hierarchically (Knill et al., 1998; Bacon et al., 1999). Engineering the environment (reservoir), and therefore decoherence, may be a way to avoid complex error-correcting schemes. Decoherence rate scales with the square of a quantity describing the amplitude of the superposition states (Myatt et al., 2000). The best solution of the problem of reservoir is a squeezed reservoir, where all initial states asymptotically relax to a squeezed state of motion (Poyatos et al., 1996), which is achieved via QND measurements.

The quantum device possesses its own potential internal quantum state (IQS), which is maintained for prolonged time via a reflective error-correction. It is a part representing a superposition of the potential contradictory reality (vacuum), i.e. it belongs to a microscale, and it is mapped to a macroscopic “body” of the device. The error-correction is a reflection over this state. It is concatenated within the 3D space as a molecular computer (MC). IQS cannot be cloned but it can exhibit itself by a creative generation of limits of iteration in the 3D world. Superpositions can exist only in quantum systems that are free from the external influences. Thus the external influence should be

restricted only to error correction without disturbing the IQS. A decay from a superposition to a statistical mixture of states is called decoherence. The rates of decoherence scale exponentially with the size of superposition.

In artificial quantum computers, which principal basis is currently under extensive theoretical consideration, the error-correction is allotted by a human constructing this device. In natural quantum computers, which are living systems, the error-correction is internal. It is a result of reflection, given as an estimation of the “state of affairs”, i.e. as a sort of an *internal process* (measurement proceeding internally) allotting optimal limits of iteration. The IQS by its internal “decision” causes decoherence being coherence-free itself. The IQS is a decoherence-free subspace, which can apply decoherence to its envelope (body). This decoherence should be error-corrected. The decoherence-free state is maintained by the error-correcting code from the quantum computer. Error-correcting code is concatenated by the encoding in genome.

The IQS is a kind of Leibniz monad and resembles the properties of a quasi-particle (see Nakagomi, 2003), which interacts with the surround, applying decoherence commands to it and maintained by the program of error-correcting codes. In this framework, enzymes are molecular automata of the extremal quantum computer, the set of which maintains highly ordered coherent state, and genome represents a concatenation of error-correcting codes into a single reflective set. Thus internal molecular quantum measurement should be coupled to appropriate emerging measurement records as molecular symbols (Pattee, 1971; Balázs, 2003).

The MC operates with molecular words (DNA, RNA) having definite addresses. The MC functions if the operator acts as an enzyme. The set of operators forms the program of calculation, where operators collide by the Brownian movement. A program can be rearranged in the course of computation. The long-term memory of the MC is based on DNA, the short-term memory—on RNA (Lieberman, 1979).

Different signals can displace a probability distribution in the IQS. Molecular computer is an input and output device of the IQS. A search of address is realized by the directed mechanical transition (Lieberman, 1983). Thus, the molecular computer maintains the IQS and governs its operation. The en-

tering (input) into the IQS should be realized by the code of a minimal influence on the system (i.e., by the error-correcting code recognizing only a wrong decision) and the code should be optimal also on the output (Lieberman, 1989).

Another, complementary to the body, projection of the IQS is a constructing of space–time image (which appears initially as a subject’s recognition of itself in the mirror). It is possible only when IQS reaches a very high capacity for decision-making. In terms of Lacan (1977), this projection includes a symbolic restriction of the ego by the imposed language (superego), which is in other words a reflection of IQS on itself by means of superego (Igamberdiev, 1999b). In this framework, the different IQSs are linked via exhibiting their objectivation and signification. Also, arising to Pythagoras and further to Leibniz, there should be a harmony of the observed world so different IQS should exist as immersed into the total whole reality. The monads have no windows, according to Leibniz, but they are synchronized via a harmonic objectivation based on the uniformity of fundamental constants. This synchronization is achieved at certain values of physical constants, which are substantiated as appearing to be a unique solution within the reflective loop, corresponding to its robust self-maintenance (Igamberdiev, 1999b, 2001).

Physical laws operating with fundamental constants represent a basis of the natural computation. They are optimized within a reflective process in such a way that allows the appearance of higher levels of reflection, including such phenomena as free will and consciousness. Biological systems, being autopoietic in physical space (Maturana, 1999) control what, when and where measurements are made on the physical universe (Pattee, 1993). The biological evolution is really a functional evolution of measurement constraints, from cells to brains (Pattee, 2001).

IQS remains robust against measurement process. Although the standard view represents the quantum wavefunction as extremely fragile against measurement (e.g. Schrödinger’s cat), the maintenance of IQS is responsible for securing the stability of the macroscopic material world. The IQS is a necessary infrastructure to uphold the material world informationally. Robustness of IQS corresponds to the physical limitation of computational process (Lieberman, 1989). Living systems are quantum regulators, which

realize encoding according to their internal choice, and the nature is constructed on the basis of the principle of minimal influence (demolition) caused by measurement and calculation.

3. Iterative exhibition of internal activity

How can we distinguish a subjective internal process from the external non-generic phenomenon? There should be something in the generated structure, which really is a limit of iteration that exhibits an internal process based on unfolding the triadic structure, which includes IQS, body and MC. Any internal (subjective) choice exhibits a structure of the semantic paradox, arising to Epimenides (Igamberdiev, 1999). The paradox results from mixing the notion of indicating an element with the act of indicating a set consisting of elements. In Gunji’s approach, a certain transition rule is used recursively along time. In order to resolve the paradox, the form of a fixed point (the point of coincidence of the image and its reflection) is identified with a domain equation and a reflective domain is obtained, however any resolution is destined to be relative. Solving and obtaining a reflective domain is used as a new transition rule (Gunji et al., 1997). A finite velocity of observation propagation collapses into fractal space–time structure. According to this approach, the fixed point x for the operation of determination of A and A^- , denoted by F can be expressed as an infinite recursion, $x = F(F(F(\dots F(x)\dots)))$, by mapping $x = F(x)$ onto $x = F(x)$. It can be considered as a point in a two-dimensional space. The operation of F is the contraction in a two-dimensional domain, indicating either A or A^- (Kitabayashi et al., 1999).

If validity of A is denoted by m , the invariance of validity with respect to contraction is expressed as $f(m) * m = \text{constant}$, where m is the value of validity and $f(m)$ is the probability of m . If distribution of $f(m)$ does not have an off-set peak, m directly means the rank. Then $f(m) * m = c$ represents what is called the Zipf’s law, i.e. $\log(f(m)) = -\log(m) + c$ (for details see Kitabayashi et al., 1999).

The similar formula was introduced by Mandelbrot (1982) for the fractal structure, actually fractal is an iteration arising from the set of complex numbers by squaring them, i.e. by reflecting them to the 2D space. An observer cannot detect the Zipf’s law until some

tool appears, which is a hyperlink between the other objects. It allows realization of the combinatorial game between the objects connected by the hyperlink. The third dimension is a reflection over this 2D domain. It appears if we estimate the actualization domain for the error-correction. This is possible only through the introduction of the internal time of observer. As a result, the 3D + T structure appears. According to the Zipf's law, the probability of occurrence of words or other items starts high and tapers off exponentially. Thus a few occur very often while many others occur rarely. The distribution of words is often an inverse exponential like e^{-an} . The power law and the fractal structure appear in the systems exhibiting quantum computation as a consequence of the reflective control.

In biological morphogenesis, the preceding motif unit F is transferred into the subsequent one by a certain fixed similarity transformation g , i.e., $F_{k+1} = g * F_k$. If we have the generating transformation g unfolding m times to a motif unit F_k , a component F_{k+m} is obtained, and a group of transformation G will contain elements $g^0, g^1, g^2, \dots, g^m$ (Petukhov, 1989). The concrete mean of g corresponds to internal timing within the reflective loop. A finite representation of measurement result forms a coordinate scale inherent to any individual morphological form. These coordinate scales can be transformed by simple recursive rules via rescaling (Thompson d'Arcy, 1917). The domains of these structures are hierarchically embedded one into another and function at every level with different clock time periods. The limit of actualization fits optimality of the structure being actualized, thus it provides the existence of optimal solutions for design.

Let take the simplest and most general way of transformation when a new domain is composed of two previous. The importance of such transformation is based on the internal evolutionary process, which includes the formation of self-referential loops. In this process, the evolving state is determined by the two (in the simplest case) contradictory values of the system separated by time interval, and the value in time future is acquired after addressing them. Addressing the fixed point means that the two contradictory statements taken as sequential values separated by time interval and equally probable are composed to get the third statement. Thus the next statement (quantitatively modeled as having correspondent value) is composed from the two previous statements when they

are memorized within the reflective loop: $F_{n+2} = F_n + F_{n+1}$. This will lead to important evolutionary consequences: in the transformation of a non-local incurative system to a local recursive system, certain recursive limits will appear as fundamental canons of perfection formed as memorization within reflective loops.

The Fibonacci series represent a recurrent consequence of values (at $n = 0, 1, 2, 3, \dots$) where n may correspond to the values at discrete times of generating and addressing the fixed point. In many cases of biological morphogenesis the following configurations (different expressions of the golden section) are realized as limits ($n \rightarrow \infty$) of infinite recursion:

$$\Phi = \lim \frac{F_{n+1}}{F_n} = \frac{(1 + 5^{1/2})}{2} = 1.618 \dots$$

$$\Phi^2 = \lim \frac{F_{n+2}}{F_n} = \frac{(3 + 5^{1/2})}{2} = 2.618 \dots$$

$$\frac{1}{\Phi} = \lim \frac{F_n}{F_{n+1}} = \frac{2}{(1 + 5^{1/2})} = 0.618 \dots$$

From these equations, it is possible to obtain the solution for F_n , which depends only on the number of addressing the fixed point (number of recursions). It will be described by the equation (Binet's Fibonacci number formula):

$$F_n = \frac{(1 + 5^{1/2})^n - (1 - 5^{1/2})^n}{2^n \times 5^{1/2}}$$

The Fibonacci numbers represent possible solutions for morphogenetic problems, as numbers of ways of picking sets in recursive process with the formation of corresponding spatial patterns (Brousseau, 1972; Honsberger, 1985). Other useful series appear when three neighboring elements F_n, F_{n+1}, F_{n+2} of the Fibonacci are taken as lengths of three sequential segments (as appeared in the sequential past ($t - 1$), present (t) and future ($t + 1$) times). In this case we get the ratio defined as the wurf and its "golden wurf" limit W (Petukhov, 1988):

$$\begin{aligned} W &= \lim \frac{(F_n + F_{n+1})(F_{n+1} + F_{n+2})}{F_{n+1}(F_n + F_{n+1} + F_{n+2})} \\ &= \frac{\Phi^2}{2} = \frac{(3 + 5^{1/2})}{4} = 1.309 \dots \end{aligned}$$

The value of golden wurf as a limit of the recursive process will have the wurf of three sequential segments with the values 1, Φ and Φ^2 , i.e. it follows from the memorization of limits of recursion in the Fibonacci series (Petukhov, 1989). The golden section and the golden wurf constants represent fundamental values of infinite recursion when the next element is formed by the operation on the two previous sequentially appearing elements memorized within the reflective loop. They always occur in morphogenetic patterns appearing as limits of infinite process of recursive embedding arising from reflective action (internal quantum measurement). The ‘golden wurf’ being the limit of lengths series of three sequential stretches divided by three neighboring numbers of the Fibonacci series, i.e., the constant characteristic for the actualized triadic structure, is even more characteristic morphological parameter than the golden section (Petukhov, 1989).

The neighboring members of the Fibonacci series are linked by the relation:

$$F_n \times F_{n+2} = F_{n+1}^2 + (-1)^n$$

Other types of transformation can be described by more complicated parameters. In many cases, since they represent reflective unfolding via separation of contradictory statements, they may be presented via incorporation of a certain defect to the system, which evolves according to the golden section rule. Following Petukhov (1988), a deviation from the symmetrical relation will be described as the incorporation of the defect Δ :

$$F_n \times F_{n+2} = F_{n+1}^2 + (-1)^n \times \Delta$$

This deviation (dissymmetrization) being internalized, can generate a higher-order symmetry at the consequent step of the evolution corresponding to a sequence of canons (Lyubishchev, 1973). The value of form is not only pragmatic: it needs aesthetic criteria, primary to any concrete adaptive harmony. A deviation from the symmetrical relation by the outside parameter will lead to a generation of a different limit of recursion, corresponding to a new configuration which fits to a certain canon. While approaching this limit, an external stimulus that caused a certain defect is internalized within the system and the system evolves to a new more complex state with a higher order symmetry relation. In this state, an uncertainty in interaction

between the system and its environment is reduced via a formation of a self-reflective loop in which a new recursive function is established. The system becomes able to perform a new high-precision internal measurement that adequately responds to a such external stimulus.

4. Reflective structure of living system

The reflective system of living beings (hypercycle) consists of catalysts, substrates and an embedded subset of substrates serving as a matrix for catalysts’ reproduction (Eigen and Schuster, 1979). In the simplest case (RNA catalysis—ribozymes), a single molecule can hold all these properties (of catalyst, its substrate, and the matrix). Gamow (1954) was the first who introduced a notion about the digital arithmetical nature of the genetic code. The code interacts with the whole reflective system as its embedded digital description, which limits its development to simple recursive rules. It is a computable part of the non-computable system similar to the set of Gödel numbers within the arithmetic system that are necessary for its description (Igamberdiev, 1998). The pattern of the genetic code could be formed on the basis of search for the optimal variant of the reflective structure. Arithmetic power of the genetic code has extremely high efficiency for information processing (Shcherbak, 2003). The code is a digital alphabet of the mobile genetic system in which the combinatorial transformations use molecular addresses at all levels of informational transfer (mobility of genome, splicing, posttranslational processing). During this process, single events corresponding to realization of interacting individual programs form a percolating network, and this leads to concrete spatial patterns constructed using optimal coordinate scales.

DNA folding leads to the formation of alternate structures (within general types of right-handed and left-handed helical) differing in curvatures and topologies that could exist in a superposition before their internal observation (measurement). DNA possesses a scale-invariant property consisting in the existence of a long-range power law correlation (Gamow and Ycas, 1955), which is expressed mostly in intron-containing genes and in non-transcribed regulatory DNA sequences (Peng et al., 1992). Combinatorial events drive the system in an out-of-equilibrium

steady state characterized by a power law size distribution (Provata, 1999). The coding part of the genome seems to have smaller fractal dimension and longer correlations, than non-coding parts (Abramson et al., 1999). Fractal properties of DNA particularly in its non-coding regions may reflect important properties for providing a combinatorial power for the developmental and evolutionary dynamics of the genetic material, particularly for specific recognitions (as in the case of enzymes) during genome rearrangements. They are connected with the existence of quasi-particles and coherent quanta inside the helical structure of DNA molecule that change their orientation during topological reconstructions and rearrangements. This may provide the existence of genome as a permanently changing superposition of potential states that are reduced in the course of interaction with the changing environment.

The genomic superposition is reduced via the transformational generative grammar of genetic texts in the sense of Chomsky (1965). The principles of generative transformations of genetic texts will form a set of interactions based on molecular addresses. Such a generative grammar is equivalent to a language game (open process) with limits (constraints).

The reflective control in genome is realized by tools (molecular addresses) organizing combinatorial events. Thus, the molecular addresses establish the set of rules for language game corresponding to such hierarchical organization. Following Head (1987), the genetic structure can be viewed as consisting of the two complementary sets. The first set consists of double-stranded DNA molecules, the second set of recombinant behaviors allowed by specific classes of enzymatic activities. The associated language consists of strings of symbols that represent the primary structures of the DNA molecules under the given enzymatic activities. By this structure, the recombinant (splicing) system possesses a generative formalism. Further Paun (1996) showed the closure to Chomsky language families under the splicing operations. The generative capacity of splicing grammar systems is provided by its components. Any linear language can be generated by a splicing grammar with two regular components. Any context-free language can be generated by a splicing grammar system with three regular components. Any recursive enumerable language can be generated by a splicing grammar

system with four regular components (Georgescu, 1997).

Artificial biocomputers using DNA have been discussed theoretically and tested experimentally (Adleman, 1994; Faulhammer et al., 2000). In living systems, natural computing process uses DNA and RNA molecules as the basis of gene processing and scrambling (Landweber et al., 2000). Computational strategies based on language games connected with combinatorial events of the genome underlie evolutionary process (Igamberdiev, 1998). The evolutionary process could evaluate the arithmetic power of the genetic code upon its development (Shcherbak, 2003). As a result, only one in every million random alternative codes is more efficient against mutation than the natural code (Freeland and Hurst, 1998), however, those codes cannot get some comparable exact order at random (Shcherbak, 2003), so the existing genetic code is a unique output based on its optimality in its digital representation of biosystem. It seems that performing arithmetic by genetic code is the most optimal, based on existing physical structure, and embodiment of digits occurs in a way of possible perfection. The computation strategy of genome is an example of self-assembly mode of computing (Conrad, 1999). The self-assembly may be realized as a computation by carving (Manca et al., 1999), which represents a computation strategy to generate a large set of candidate solutions of a problem, then remove the non-solutions such that what remains is the set of solutions. This is the strategy of error-correction in the potential field.

The reality can be described as a set of self-maintained reflective systems exhibiting themselves externally (on macroscales) and interacting via perpetual process of signification (reducing the microscale), which introduces universal computable laws harmonizing their interaction. The evolutionary growth of information occurs via language game of interacting programs, an open process without frames. The solutions coming to existence are based on the most optimal way for physical embodiment of computing process, and this is in line with Leibniz's notion about the most perfect world among all possible, which corresponds to contemporary formulations of the anthropic principle. Possessing free will and consciousness, we may accept this world as a suitable place for living or reject it (i.e. express optimistic or

pessimistic ethical view), but its mathematically formulated physical parameters may strictly correspond to its observability by embodied living organisms having internal digital structure with alphabet and grammar, which generates a unique solution for the appearance of free will and consciousness.

References

- Abramson, G., Cerdeira, H.A., Bruschi, C., 1999. Fractal properties of DNA walks. *BioSystems* 49, 63–70.
- Ahn, C., Wiseman, H.M., Milburn, G.J., 2003. Quantum error correction for continuously detected errors. *Phys. Rev. A* 67, 052310.
- Adleman, L.M., 1994. Molecular computation of solutions to combinatorial problems. *Science* 266, 1021–1023.
- Bacon, D., Lidar, D.A., Whaley, K.B., 1999. Robustness of decoherence-free subspaces for quantum computation. *Phys. Rev. A* 60, 1944–1955.
- Balázs, A., 2003. On the physics of the symbol-matter problem in biological systems and the origin of life: affine Hilbert spaces model of the robustness of the internal quantum dynamics of biological systems. *BioSystems* 70, 43–54.
- Bennett, C.H., 1979. Dissipation-error tradeoff in proofreading. *BioSystems* 11, 85–91.
- Blumenfeld, L.A., 1983. *Physics of Bioenergetic Processes*. Springer-Verlag, Berlin.
- Braginsky, V.B., Khalili, F.Y., 1996. Quantum non-demolition measurements: the route from toys to tools. *Rev. Modern Phys.* 68, 1–11.
- Braginsky, V.B., Vorontsov, Y.I., Thorne, K.S., 1980. Quantum non-demolition measurements. *Science* 209, 547–557.
- Brousseau, A., 1972. Fibonacci numbers and geometry. *Fibonacci Quarter.* 10, 303–318.
- Chomsky, N., 1965. *Aspects of the Theory of Syntax*. MIT Press, Cambridge, MA.
- Conrad, M., 1999. Molecular and evolutionary computation: the tug of war between context freedom and context sensitivity. *BioSystems* 52, 99–110.
- Conrad, M., Liberman, E.A., 1982. Molecular computing as a link between biological and physical theory. *J. Theor. Biol.* 98, 239–252.
- Eigen, M., Schuster, P., 1979. *The Hypercycle: A Principle of Natural Self-Organization*. Springer-Verlag, Berlin.
- Elsasser, W., 1982. The other side of molecular biology. *J. Theor. Biol.* 96, 67–76.
- Facchi, P., Pascazio, S., 2002. Quantum Zeno subspaces. *Phys. Rev. Lett.* 89, 080401.
- Faulhammer, D., Cukras, A.R., Lipton, R.J., Landweber, L.F., 2000. Molecular computation: RNA solutions to chess problems. *Proc. Natl. Acad. Sci. U.S.A.* 97, 1385–1389.
- Freeland, S.J., Hurst, L.D., 1998. The genetic code is one in a million. *J. Mol. Evol.* 47, 238–248.
- Gamow, G., 1954. Possible relation between deoxyribonucleic acid and protein structure. *Nature* 173, 318.
- Gamow, G., Ycas, M., 1955. Statistical correlation of protein and ribonucleic acid composition. *Proc. Natl. Acad. Sci. U.S.A.* 41, 1011–1019.
- Gea-Banacloche, J., 2000. Quantum codes and macroscopic superpositions. *Phys. Rev. A* 6102, 2302.
- Georgescu, G., 1997. On the generative capacity of splicing grammar systems. *New Trends Formal Languages* 1218, 330–345.
- Gunji, Y.-P., Ito, G., 1999. Orthomodular lattice obtained from addressing a fixed point. *Physica D* 126, 261–274.
- Gunji, Y.-P., Ito, K., Kusunoki, Y., 1997. Formal model of internal measurement: alternate changing between recursive definition and domain equation. *Physica D* 110, 289–312.
- Hameroff, S.R., 1994. Quantum coherence in microtubules: a neural basis for emergent consciousness. *J. Consc. Studies.* 1, 91–118.
- Hameroff, S.R., Penrose, R., 1996. Conscious events as orchestrated spacetime selections. *J. Consc. Studies* 3, 36–53.
- Hameroff, S., Nip, A., Porter, M., Tuszynski, J., 2002. Conduction pathways in microtubules, biological quantum computation, and consciousness. *BioSystems* 64, 149–168.
- Harada, Y., Sakurada, K., Aoki, T., Thomas, D.D., Yanagida, T., 1990. Mechanical coupling in actomyosin energy transduction studied by in vitro movement assay. *J. Mol. Biol.* 216, 49–68.
- Head, T., 1987. Formal language theory and DNA: an analysis of the generative capacity of specific recombinant behaviors. *Bull. Math. Biol.* 49, 737–759.
- Honsberger, R., 1985. *A Second Look at the Fibonacci and Lucas Numbers, in Mathematical Geometry*. Mathematical Association of America, Washington DC.
- Igamberdiev, A.U., 1993. Quantum mechanical properties of biosystems: a framework for complexity, structural stability and transformations. *BioSystems* 31, 65–73.
- Igamberdiev, A.U., 1998. Time, reflectivity and information processing in living systems: a sketch for the unified informational paradigm in biology. *BioSystems* 46, 95–101.
- Igamberdiev, A.U., 1999a. Foundations of metabolic organization: coherence as a basis of computational properties in metabolic networks. *BioSystems* 50, 1–16.
- Igamberdiev, A.U., 1999b. Semiosis and reflectivity in life and consciousness. *Semiotica* 123, 231–246.
- Igamberdiev, A.U., 2001. Semiokinesis—semiotic autopoiesis of the Universe. *Semiotica* 133, 1–26.
- Igamberdiev, A.U., 2003. Living systems are dynamically stable by computing themselves at the quantum level. *Entropy* 5, 76–87.
- Kitabayashi, N., Kusunoki, Y., Gunji, Y.-P., 1999. The emergence of the concept of tool in food-retrieving behavior of the ants *Formica japonica* Motschulsky. *BioSystems* 50, 143–156.
- Knill, E., Laflamme, R., Zurek, W.H., 1998. Resilient quantum computation. *Science* 279, 342–345.
- Lacan, J., 1977. *Écrits*. W.W. Norton, N.Y. (Sheridan, A., Trans.; original work published in 1966).
- Landweber, L.F., Kuo, T.-C., Curtis, E., 2000. Evolution and assembly of an extremely scrambled gene. *Proc. Natl. Acad. Sci. U.S.A.* 97, 1385–1389.
- Leibniz, G.W., 1965. *Monadology and Other Philosophical Essays*, Bobbs-Merrill, Indianapolis (Schrecker, P., Schrecker, A.M. Schrecker, P. (Eds.), Trans.; original work published in 1714).

- Liberman, E.A., 1979. Analog-digital molecular cell computer. *BioSystems* 11, 111–124.
- Liberman, E.A., 1983. Extremal molecular quantum regulator. *Biofizika* 28, 183–185.
- Liberman, E.A., 1989. Molecular quantum computers. *Biofizika* 34, 913–925.
- Liberman, E.A., Minina, S.V., Shklovsky-Kordi, N.E., 1986. Role of electro-mechanical and reaction-diffusional system of intraneuronal information processing in brain function. *Biofizika* 31, 298–303.
- Lyubishchev, A.A., 1973. The letter to N.G. Kholodny. *Priroda* No 10, 46 [in Russian].
- Manca, V., Martín-Vide, C., Paun, G., 1999. New computing paradigms suggested by DNA computing: computing by carving. *BioSystems* 52, 47–54.
- Mandelbrot, B.B., 1982. *The Fractal Geometry of Nature*. Freeman, San Francisco.
- Marijuán, P.C., Westley, J., 1992. Enzymes as molecular automata: a reflection on some numerical and philosophical aspects of the hypothesis. *BioSystems* 27, 97–113.
- Matsuno, K., 1993. Being free from *Ceteris Paribus*: a vehicle for founding physics on biology rather than the other way around. *Appl. Math. Comput.* 56, 261–279.
- Matsuno, K., 1995. Quantum and biological computation. *BioSystems* 35, 209–212.
- Matsuno, K., 1999. Cell motility as an entangled quantum coherence. *BioSystems* 51, 15–19.
- Matsuno, K., Paton, R.C., 2000. Is there a biology of quantum information? *BioSystems* 55, 39–46.
- Maturana, H.R., 1999. The organization of the living: a theory of the living organization. *Int. J. Hum.—Computer Studies* 51, 149–168.
- Myatt, C.J., King, B.E., Turchette, Q.A., Sackett, C.A., Kielpinski, D., Itano, W.M., Monroe, C., Wineland, D.J., 2000. Decoherence of quantum superpositions through coupling to engineered reservoirs. *Nature* 403, 269–273.
- Nakagomi, T., 2003. Mathematical formulation of Leibnizian world: a theory of individual-whole or interior-exterior effective systems. *BioSystems* 69, 15–26.
- Nielsen, M.A., 2003. Quantum computation by measurement and quantum memory. *Phys. Lett. A* 308, 96–100.
- Pattee, H.H., 1971. Can life explain quantum mechanics? In: Bastin, T. (Ed.), *Quantum Theory and Beyond*. Cambridge University Press, Cambridge, pp. 307–319.
- Pattee, H.H., 1993. The limitations of formal models of measurement, control and cognition. *Appl. Math. Comput.* 56, 111–130.
- Pattee, H.H., 2001. The physics of symbols: bridging the epistemic cut. *BioSystems* 60, 5–21.
- Paun, G., 1996. On the splicing operation. *Discrete Appl. Math.* 70, 57–79.
- Peng, C.K., Buldyrev, S.V., Goldberger, A.L., Havlin, S., Sciortino, F., Simons, M., Stanley, H.E., 1992. Long range correlations in nucleotide sequences. *Nature* 356, 168–170.
- Petukhov, S.V., 1988. Higher symmetries, transformations and invariants in biological objects. In: Tyukhtin, V.S., Urmantsev, Y.A. (Eds.), *System, Symmetry, Harmony*. Mysl', Moscow [in Russian], pp. 260–274.
- Petukhov, S.V., 1989. Non-Euclidean geometries and algorithms of living bodies. *Comput. Math. Appl.* 17, 505–534.
- Poyatos, J.F., Cirac, J.I., Zoller, P., 1996. Quantum reservoir engineering with laser cooled trapped ions. *Phys. Rev. Lett.* 77, 4728–4731.
- Provata, A., 1999. Random aggregation models for the formation and evolution of coding and non-coding DNA. *Physica A* 264, 570–580.
- Raussendorf, R., Briegel, H.J., 2001. A one-way quantum computer. *Phys. Rev. Lett.* 86, 5188–5191.
- Raussendorf, R., Browne, D.E., Briegel, H.J., 2003. Measurement-based quantum computation on cluster states. *Phys. Rev. A* 68, 022312.
- Rosen, R., 1977. Observation and biological systems. *Bull. Math. Biol.* 39, 663–678.
- Shcherbak, V.I., 2003. Arithmetic inside the universal genetic code. *BioSystems* 70, 187–209.
- Thompson d'Arcy, W., 1917. *On Growth and Form*. Cambridge University Press, London.
- van der Meyden, R., Patra, M., 2003. A logic for probability in quantum systems. *Lect. Not. Comput. Sci.* 2803, 427–440.